Outline

• The Metabolomics Innovation Centre (TMIC)
• Metabolomics for food analysis
• Alberta Food Composition Project
• Food and Metabolomics Databases
• Metabolomics in livestock analysis
• Conclusions
The Metabolomics Innovation Centre

Comprehensive, Quantitative Metabolomics Services

www.metabolomicscentre.ca
Established in 2011, funded by Genome Canada to meet Canada’s growing demand for high quality, high throughput metabolomic services.

TMIC is Canada’s national metabolomics laboratory and national metabolomics technology demonstration centre (MTDC).

>$30 million in equipment distributed across 4 nodes at the UofA, 1 node at UVic, 1 node at McGill, 1 node at McMaster -- 30 staff and trainees.

Accounts for 80% of Canada’s metabolomics publications.

www.metabolomicscentre.ca
Leadership

Dr. Christoph Borchers, Co-Director, UVic & McGill
Dr. David Wishart, Director, UofA
Dr. Liang Li, Core Scientist, UofA
Dr. James Harynuk, Core Scientist, UofA
Dr. Philip Britz-McKibbin, Core Scientist, McMaster
Dr. Michael Overduin, Core Scientist, UofA
A Distributed Centre
The Metabolomics Innovation Centre (TMIC) - Comprehensive and Quantitative Metabolomics

November 16, APC Forum, UCC
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Some Definitions

• Food Composition Analysis – The determination of the chemical (metabolite) components in food

• Food Biomarkers – Food components or food metabolites found in the metabolome that are characteristic of specific foods

• Metabolomics – The high throughput analysis and characterization of the chemicals constituting the metabolome
Food Component Analysis

Traditional

- Protein
- Fat
- Ash
- Minerals
- Carbohydrates
- Calories
- Water content

Metabolomics

- Alanine
- Tryptophan
- Methyl-histidine
- PE(18:0/18:2)
- PE(16:0/18:1)
- TG(16:0/16:0/18:0)
- Phosphate
- Calcium
- Zinc
- Fructose
- Glucose
- N-acetylglucosamine
- Apigenin
- Gallic acid
- Resveratrol
- Epigallocatechin Gallate
- Proline betaine
- ....
The Metabolomics Workflow

1. Biological or Tissue Samples
2. Extraction
3. Biofluids or Extracts
4. Data Analysis
5. Chemical Analysis
Metabolomics Technologies

- UPLC, HPLC
- CE/microfluidics
- GC-MS
- LC-MS
- LC-MS/MS
- ICP-MS
- NMR spectroscopy
- X-ray crystallography
- FTIR
Technology & Sensitivity

# Metabolites detected (Log_{10})

- Known unknowns
- Unknown unknowns

Sensitivity or LDL

- NMR
- GC-MS
- TOF
- Quad

LC-MS or DI-MS
Metabolomics for Food Analysis

Food Samples → Extraction → Food Extracts

Data Analysis → Chemical Analysis
Advantages of Metabolomics

- Applicable to food composition analysis and food biomarker analysis
- Uses rapid, high throughput methodologies (robotics, UPLC, MS/MS)
- Offers exquisite sensitivity (< 1 nM)
- Can be absolutely quantitative
- Can detect 100s to 1000s of compounds vs. only 10’s for conventional methods
## WineScreener & JuiceScreener

![Bruker BioSpin ($600,000)](image)

<table>
<thead>
<tr>
<th>Compound</th>
<th>Value</th>
<th>Unit</th>
<th>Official Reference Flag</th>
<th>Wine-Profiling™ Authentic NMR Database</th>
</tr>
</thead>
<tbody>
<tr>
<td>acetic acid</td>
<td>525</td>
<td>mg/L</td>
<td>0 mg/L</td>
<td>1007</td>
</tr>
<tr>
<td>benzoic acid</td>
<td>&lt;5</td>
<td>mg/L</td>
<td>0 mg/L</td>
<td>&lt;5 mg/L in reference set</td>
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<tr>
<td>citric acid</td>
<td>299</td>
<td>mg/L</td>
<td>1000 mg/L</td>
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<tr>
<td>ethanol</td>
<td>91.7</td>
<td>g/L</td>
<td>108.0</td>
<td>56.2</td>
</tr>
<tr>
<td>fumaric acid</td>
<td>&lt;5</td>
<td>mg/L</td>
<td>12</td>
<td>&lt;200</td>
</tr>
<tr>
<td>glycerol</td>
<td>7.1</td>
<td>g/L</td>
<td>11.1</td>
<td>&lt;5 mg/L in reference set</td>
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<tr>
<td>malic acid</td>
<td>5.5</td>
<td>g/L</td>
<td>8.2</td>
<td>&lt;0.2</td>
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<tr>
<td>methanol</td>
<td>53</td>
<td>mg/L</td>
<td>146</td>
<td>6</td>
</tr>
<tr>
<td>shikimic acid</td>
<td>88</td>
<td>mg/L</td>
<td>100</td>
<td>&lt;20</td>
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<tr>
<td>sorbic acid</td>
<td>&lt;5</td>
<td>mg/L</td>
<td>107</td>
<td>&lt;5 mg/L in reference set</td>
</tr>
</tbody>
</table>
Milk Metabolomics

• The Chemical Composition of Cow’s Milk
• Skim milk, 1%, 2% and 3.25%
• Applied a combination of modern, quantitative metabolomics techniques along with state-of-the-art, computer-aided literature mining techniques to obtain the most comprehensive and up-to-date characterization of the chemical constituents in cow’s milk
• NMR, GC-MS, ICP-MS, LC-MS/MS, GC-FAMEs
# Milk Metabolomics

The total number of metabolites is greater than 470.

<table>
<thead>
<tr>
<th>Assays</th>
<th>No. of Metabolites</th>
</tr>
</thead>
<tbody>
<tr>
<td>NMR</td>
<td>39</td>
</tr>
<tr>
<td>DI/LC-MS/MS</td>
<td>116</td>
</tr>
<tr>
<td>ICP-MS (metals)</td>
<td>32</td>
</tr>
<tr>
<td>HPLC (vitamins)</td>
<td>12</td>
</tr>
<tr>
<td>GC-MS</td>
<td>30</td>
</tr>
<tr>
<td>Text Mining</td>
<td>255</td>
</tr>
</tbody>
</table>

**Total No. metabolites**: > 470

Manuscript preparation in progress
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The Alberta Food Composition Project

• A 5 year metabolomics project aimed at measuring the chemical composition of ~50 Alberta-grown food products (meat, poultry, dairy, cereals, oils, vegetables & fruits)

• Measuring 100’s of compounds via quantitative metabolomics techniques

• Intent is to extend and validate literature-based composition data and identify candidate food biomarkers
## Using Multiple Platforms

<table>
<thead>
<tr>
<th>Type</th>
<th>Model</th>
</tr>
</thead>
<tbody>
<tr>
<td>NMR</td>
<td>Bruker 700 MHz cryoprobe &amp; autosampler</td>
</tr>
<tr>
<td>NMR</td>
<td>Varian/Agilent 600 MHz</td>
</tr>
<tr>
<td>ICP-MS</td>
<td>Perkin Elmer NexION 350</td>
</tr>
<tr>
<td>GC-MS</td>
<td>2x Agilent 7890A GC-MS with autosampler</td>
</tr>
<tr>
<td>GC-MS</td>
<td>Agilent/HP Series 5890 GC-MS</td>
</tr>
<tr>
<td>LC-MS</td>
<td>Bruker 9.4T FT-ICR MS w. cap HPLC</td>
</tr>
<tr>
<td>LC-MS</td>
<td>2x ABI Qtrap 4000 MS w. Turbo ESI</td>
</tr>
<tr>
<td>LC-MS</td>
<td>Agilent LC-ESI ToF MS</td>
</tr>
<tr>
<td>LC-MS</td>
<td>2x Bruker maXis II qTOF</td>
</tr>
<tr>
<td>HPLC</td>
<td>Agilent w. Fluorescent detector</td>
</tr>
<tr>
<td>UPLC</td>
<td>2x Agilent 1290 Infinity UPLC</td>
</tr>
</tbody>
</table>

[www.metabolomicscentre.ca](http://www.metabolomicscentre.ca)
Typical Results

• ~50 water-soluble metabolites by NMR
• ~80 compounds by DFI/LC-MS/MS via the Biocrates AbsoluteIDQ™ kit
• ~400 lipids and fatty acids via GC-MS/LC-MS
• 53 trace elements by ICP-MS
• 48 small metabolites via GC-MS
• 17 polyphenols
• 9 water- and lipid-soluble vitamins
• Identification & quantification of ~600 cmpds
Metabolomics of Beet Root

**METHOD**

- **HPLC**: Polyphenols, vitamins, chlorophylls, anthocyanins (34)
- **NMR**: Organic acids, amino acids, amines, sugars, polyols (37)
- **GCMS**: Organic acids, amino acids, fatty acids (26)
- **GCMS (volatiles)**: Volatile organics, thiols, ketones, esters (41)
- **ICPMS**: Metals (38)
- **DIMS**: Carnitines, amino acids, phospholipids, amines (85)
- **Lipidomics**: Neutral lipids, cholesterol, phytosterols, fatty acids (~400)

**Numbers of Quantified Compounds**
The Alberta Food Composition Database (AFCDB) is the first comprehensive resource on food constituents, chemistry and biology dedicated to major Alberta-grown produce. It provides information on both macronutrients and micronutrients, including many of the constituents that give foods their flavor, color, taste, texture and aroma. Users can view the contents of the AFCDB from the “FoodView” (listing foods by their chemical composition) or the “ChemView” (listing chemicals by their food sources).

Each food entry includes a scientific name, description, and classification, as well as a list of the compounds identified with their structure, concentration range, average concentration, and references. Each chemical entry in the AFCDB contains over 70 fields of associated data, including classification, chemical properties, biological effects and interactions, spectra, and associated foods. Food constituents have been derived both from extensive literature searches and experimental data. Metabolomic profiling utilizing a combination of MS, NMR and HPLC-based techniques allowed the identification and quantification of several hundred metabolites in each food, including a number of new metabolites previously unmeasured for these Alberta-grown vegetables and fruits.

Currently, the AFCDB contains more than 30 foods and over 1700 metabolites, some of which have been identified, quantified and reported for the very first time.

Citing the Alberta Food Composition Database

AFCDB is offered to the public as a freely available presrcource. Use and re-distribution of the data, in whole or in part, for commercial purposes requires explicit permission of the authors and explicit acknowledgment of the source material (AFCDB).
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The Food Database (FooDB)

- 26,619 compounds, 25,579 structures with 24,843 descriptions
- 171,359 synonyms
- ~700,000 concentration values
- 31,791 references
- 1376 cmpds with health effects
- 2692 cmpds with flavour data
- Content data on 907 raw or processed foods
- Supports structure & text searches
- >100 data fields/compound
- Full data downloads

www.foodb.ca
Bovine Metabolome Database

• ~ 8000 compounds
• Supports structure & text searches
• >100 data fields/compound
• Full data downloads

http://www.cowmetdb.ca
The Human Metabolome Database (HMDB)

- Comprehensive database of human metabolites found in biofluids or tissues (Version 4 released in 2017)
- Old version had 41,993 metabolites, new version has 114,100 “quantified”, “detected”, “expected” and “predicted” metabolites
- Old version had 442 biological pathways, new version has 26,515
- New version has >200,000 MS/MS spectra at multiple collision energies
- New version has 5200 metabolite-SNP interactions
- Supports sequence, spectral, structure and text searches as well as compound browsing

http://www.hmdb.ca
Abstract

Metabolomics uses advanced analytical chemistry techniques to comprehensively measure large numbers of small molecule metabolites in cells, tissues and biofluids. The ability to rapidly detect and quantify hundreds or even thousands of metabolites within a single sample is helping scientists paint a far more complete picture of system-wide metabolism and biology. Metabolomics is also allowing researchers to focus on measuring the end-products of complex, hard-to-decipher genetic, epigenetic and environmental interactions. As a result, metabolomics has become an increasingly popular "omics" approach to assist with the robust phenotypic characterization of humans, crop plants and model organisms. Indeed, metabolomics is now routinely used in biomedical, nutritional and crop research. It is also being increasingly used in livestock research and livestock monitoring. The purpose of this systematic review is to quantitatively and objectively summarize the current status of livestock metabolomics and to identify emerging trends, preferred technologies and important gaps in the field. In conducting this review we also critically assessed the applications of livestock metabolomics in key areas such as animal health assessment, disease diagnosis, bioprodut characterization and biomarker discovery for highly desirable economic traits (i.e., feed efficiency, growth potential and milk production). A secondary goal of this critical review was to compile data on the known composition of the livestock metabolome (for 5 of the most common livestock species namely cattle, sheep, goats, horses and pigs). These data have been made available through an open access, comprehensive livestock metabolome database (LMDB, available at http://www.lmdb.ca). The LMDB should enable livestock researchers and producers to conduct more targeted metabolomic studies and to identify where further metabolome coverage is needed.
Livestock Metabolome Database (LMDB)

- Comprehensive database of bovine, porcine, equine, ovine, caprine metabolomic data
- 1070 metabolites
- 33 different biofluids
- 3234 concentration entries
- 15,750 NMR & MS spectra
- 616 references
- Fully searchable

http://lmdb.ca/
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Experiencing the effects of Pasture and Conventional indoor TMR cow feeding systems on the rumen and milk metabolomes

Study Design:
54 Friesian Cows

- Herd 1 (n=18): Perennial-Rye Grass ~18 kg DM/day
- Herd 2 (n=18): Perennial-Rye/20% White Clover Pasture ~18 kg DM/day
- Herd 3 (n=18): Total Mixed Ration 7.15 kg of grass silage, 7.15 kg of maize silage, and 8.3 kg concentrates /day
Impact of feeding system on the metabolome of bovine bio-fluids

Preliminary Results indicate:

• The rumen and milk metabolomes from each of the feeding systems are quite diverse and distinctive.
• NMR metabolomic profiling of milks and rumen sample
• CLV feeding system resulted in increased concentrations of formate, a substrate compound for methanogenesis. Milks and rumen-fluids were shown to have varying levels of dimethyl sulfone in each feeding system and was found to be an important compound for distinguishing between diets.
• CLV and GRS feeding systems were found to have increased concentrations of \( p \)-cresol
• This study has highlighted that \(^1\text{H-NMR}\) is capable of distinguishing both rumen-fluids and milk samples based on feeding system, which could offer potential as a tool for milk verification purposes in the future.
Current Collaboration

Tom O’Callaghan
Catherine Stanton

Scores Plot

Manuscript in preparation
Recombinant Incretin-Secreting Microbe Improves Metabolic Dysfunction in High-Fat Diet Fed Rodents

Paul M. Ryan\(^1,2\), Elaine Patterson\(^1\), Robert M. Kent\(^1,2\), Helena Stack\(^3\), Paula M. O’Connor\(^3,2\), Kiera Murphy\(^2\), Veronica L. Peterson\(^2\), Rupasri Mandal\(^5\), David S. Wishart\(^6,7,8\), Timothy G. Dinan\(^9,9\), John F. Cryan\(^9,9\), Randy J. Seeley\(^10\), Catherine Stanton\(^1,3\) & R. Paul Ross\(^1,3\)

The gut hormone glucagon-like peptide (GLP)-1 and its analogues represent a new generation of anti-diabetic drugs, which have also demonstrated propensity to modulate host lipid metabolism. Despite this, drugs of this nature are currently limited to intramuscular administration routes due to intestinal degradation. The aim of this study was to design a recombinant microbial delivery vector for a GLP-1 analogue and assess the efficacy of the therapeutic in improving host glucose, lipid and cholesterol metabolism in diet induced obese rodents. Diet-induced obese animals received either Lactobacillus paracasei NFBC 338 transformed to express a long-acting analogue of GLP-1 or the isogenic control microbe which solely harbored the pNZ4 plasmid. Short-term GLP-1 microbe intervention in rats reduced serum low density lipoprotein cholesterol, triglycerides and triglyceride-rich lipoprotein cholesterol substantially. Conversely, extended GLP-1 microbe intervention improved glucose dependent insulin secretion, glucose metabolism and cholesterol metabolism, compared to the high-fat control group. Interestingly, the microbe significantly attenuated the adiposity associated with the model and altered the serum lipidome, independently of GLP-1 secretion. These data indicate that recombinant incretin-secreting microbes may offer a novel and safe means of managing cholesterol metabolism and diet induced dyslipidaemia, as well as insulin sensitivity in metabolic dysfunction.
Predicting Dairy Cattle Disease Before Parturition

- 30-50% of dairy cows are affected by mastitis, metritis, ketosis and milk fever during transition
- 100,000 dairy cows culled/yr because of these conditions ($200 million in losses)
- Looked at serum from 12 dairy cows (-4 weeks, -1 week, +1 week, +4 weeks) during the transition period
- 6 developed diseases at +1-+3 weeks, the other 6 stayed healthy
Results (Serum Metabolomics)

VIP scores

Sensitivity (True positive rate)

1 - Specificity (False positive rate)

Area under the curve (AUC) = 0.95
95% CI: 0.892 - 0.986

- Empirical
- Smoothed
- 95% CI
Characterizing Ruminal Fluid
Fig. 1 Typical 500 MHz $^1$H-NMR rumen fluid spectra (0–9 ppm) from dairy cows fed 0% (a), 15% (b), 30% (c), and 45% (d) barley grain. Numbers indicate metabolites, as follows: 1, acetate; 2, propionate; 3, butyrate; 4, valerate; 5, isovalerate; 6, DSS; 7, 3-phenylpropionate; 8, alanine; 9, isoleucine; 10, glucose; 11, proline; 12, isobutyrate; 13, phenylacetate; 14, glycine; 15, cadaverine; 16, aspartate; 17, ethanol; 18, leucine; 19, succinate; 20, glutamate; 21, methyamine; 22, lactate; 23, choline; 24, fumarate; 25, acetone; 26, isopropanol; 27, 3-hydroxybutyrate; 28, acetoacetate; 29, 3-hydroxyphenylacetate; 30, N-nitrosodimethylamine; 31, methanol; 32, valine; 33, lysine; 34, dimethylamine; 35, glycerol; 36, maltose; 37, imidazole; 38, formate; 39, uracil; 40, nicotinate; 41, tyrosine; 42, benzoate; 43, histidine; 44, hypoxanthine; 45, phenylacetylglucose; 46, xanthine; 47, ribose. The intensity of the aromatic region (5.1–9.0 ppm) is 4 times higher than that of the aliphatic one (0.0–4.2 ppm).
The Bovine Ruminal Fluid Metabolome
..., R Mandal, SM Dunn, BN Ametaj, DS Wishart - Metabolomics, 2013 - Springer
Abstract The rumen is a unique organ that serves as the primary site for microbial fermentation of ingested plant material for domestic livestock such as cattle, sheep and goats. The chemical composition of ruminal fluid is thought to closely reflect the healthy/...

Applications of NMR in Dairy Research
AD Maher, SJ Rochfort - Metabolites, 2014 - mdpi.com
... subclinical ketosis. J. Dairy Sci., in press. 47. Saleem, F.; Bouatra, S.; Guo, AC; Psychogios, N.; Mandal, R.; Dunn, SM; Ametaj, BN; Wishart, DS The bovine ruminal fluid metabolome. Metabolomics 2013, 9, 360–378. 48. Wishart, DS ...

A metabolomics approach to uncover the effects of grain diets on rumen health in dairy cows
..., R Mandal, Q Zebeli, SM Dunn, DS Wishart - Journal of dairy ..., 2012 - Elsevier
Dairy cows fed high-grain diets during early lactation have a high incidence of metabolic disorders. However, the precise mechanism (s) of how grain feeding causes disease is not clear. In an effort to understand how this diet transition alters the rumen environment ...

Metabolomics reveals unhealthy alterations in rumen metabolism with increased proportion of cereal grain in the diet of dairy cows
..., N Psychogios, MJ Lewis, SM Dunn, J Xia, DS Wishart - Metabolomics, 2010 - Springer
Abstract This study presents the first application of metabolomics to evaluate changes in rumen metabolites of dairy cows fed increasing proportions of barley grain (i.e., 0, 15, 30, and 45% of diet dry matter). 1 H-NMR spectroscopy was used to analyze rumen fluid samples ...
Predicting Feeding Efficiency

Plasma metabolites associated with residual feed intake and other productivity performance traits in beef cattle

B.K. Karisa a, J. Thomson a,1, Z. Wang a, C. Li a,b, Y.R. Montanholi c, S.P. Miller c, S.S. Moore a,2, G.S. Plastow a,*

a Department of Agriculture, Food and Nutritional Science, 4.10 Agriculture Forestry Center, University of Alberta, Edmonton, Alberta, Canada T6G2P5
b Agriculture and Agri-Food Canada, Lacombe Research Centre, 6000 C&E Trail, Lacombe, Alberta, Canada T4L 1W1
c Centre for Genetic Improvement of Livestock, Department of Animal & Poultry Science, University of Guelph, Guelph, Ontario, Canada N1G 2W1

Epublished on May 1, 2014
Residual Feed Intake

- Measure of feed efficiency & metabolism
- Defined as the difference between an animal's actual feed intake and its expected feed intake based on its size and growth
- The lower the value, the more efficient the animal
- Moderate heritability, affected by metabolites
Fig. 1. Average concentrations of significant metabolites in the discovery population in periods 1(A), 2(B) and 3(C).
Predictive Plasma Metabolites

<table>
<thead>
<tr>
<th>Metabolite</th>
<th>Partial $R^2$</th>
<th>$P$-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Valine</td>
<td>0.30</td>
<td>0.003</td>
</tr>
<tr>
<td>Creatinine</td>
<td>0.26</td>
<td>0.021</td>
</tr>
<tr>
<td>Choline</td>
<td>0.16</td>
<td>0.008</td>
</tr>
<tr>
<td>Uridine</td>
<td>0.09</td>
<td>0.004</td>
</tr>
<tr>
<td>Histidine</td>
<td>0.08</td>
<td>0.025</td>
</tr>
<tr>
<td>Dimethylamine</td>
<td>0.03</td>
<td>0.048</td>
</tr>
<tr>
<td>Trimethylamine</td>
<td>0.03</td>
<td>0.023</td>
</tr>
<tr>
<td>2-Hydroxybutyrate</td>
<td>0.02</td>
<td>0.044</td>
</tr>
<tr>
<td>3-Hydroxybutyrate</td>
<td>0.02</td>
<td>0.005</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>0.99</strong></td>
<td></td>
</tr>
</tbody>
</table>
Predictive Plasma Metabolites

Table 3
Metabolites significantly associated with variation in dry matter intake (DMI) in the validation population of beef cattle in period 1 (2 weeks into the feeding trial).

<table>
<thead>
<tr>
<th>Metabolite</th>
<th>Partial $R$-square</th>
<th>Model $R$-square</th>
<th>$P$-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fumarate</td>
<td>0.39</td>
<td>0.39</td>
<td>0.003</td>
</tr>
<tr>
<td>Pyroglutamate</td>
<td>0.17</td>
<td>0.56</td>
<td>0.018</td>
</tr>
<tr>
<td>Choline</td>
<td>0.14</td>
<td>0.70</td>
<td>0.016</td>
</tr>
<tr>
<td>Creatinine</td>
<td>0.13</td>
<td>0.83</td>
<td>0.003</td>
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<tr>
<td>Ornithine</td>
<td>0.09</td>
<td>0.92</td>
<td>0.001</td>
</tr>
<tr>
<td>HIB</td>
<td>0.02</td>
<td>0.94</td>
<td>0.035</td>
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<tr>
<td>Dimethylamine</td>
<td>0.02</td>
<td>0.96</td>
<td>0.034</td>
</tr>
<tr>
<td>Trimethylamine</td>
<td>0.01</td>
<td>0.97</td>
<td>0.054</td>
</tr>
<tr>
<td>Methylxoxovalerate</td>
<td>0.01</td>
<td>0.98</td>
<td>0.050</td>
</tr>
<tr>
<td>Malate</td>
<td>$&lt; 0.01$</td>
<td>0.98</td>
<td>0.025</td>
</tr>
<tr>
<td>Glucose</td>
<td>$&lt; 0.01$</td>
<td>0.98</td>
<td>0.036</td>
</tr>
<tr>
<td>Citrate</td>
<td>$&lt; 0.01$</td>
<td>0.98</td>
<td>0.050</td>
</tr>
</tbody>
</table>
Conclusions

- Metabolomics is transforming food composition analysis
- Food composition databases have grown considerably in depth and breadth thanks to metabolomics
- Quantitative metabolomics is leading to the identification of dozens of new and useful food biomarkers
- Metabolomics is transforming crop and livestock research and agriculture practice
Acknowledgements

• Augustin Scalbert
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• Reza Jafari
• Naama Karu

• Ana Marcu
• An Chi Guo
• Edison Dong
• FoodBall Team

[Logos of Genome Alberta, Genome Canada, TMIC, The Metabolomics Innovation Centre, and FoodBall: The Food Biomarker Alliance]